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OM protein - protein search, using sw model

Run on: August 22, 2003, 15:07:34 ; Search time 24 Seconds  
(without alignments)  
685.806 Million cell updates/sec

Title: US-09-745-506-37  
Perfect score: 350  
Sequence: 1 MDKALSLNDPASTSPAE.....LENKINILITSETRDPLQVY 350

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	350	100.0	350	NEFL_HUMAN	09gzt8 homo sapien
2	51	14.6	350	NEFL_MOUSE	09gzt8 mus musculu
3	10	2.9	366	YF59_STAM	09gzt7 staphylococ
4	9	2.6	288	NIF3_YEAST	091081 saccharomyc
5	7	2.0	119	RNPA_MYCPA	091719 mycobacteri
6	7	2.0	146	SSBS_XENLA	P09380 xenopus lae
7	7	2.0	148	SSBR_XENLA	P09381 xenopus lae
8	7	2.0	150	COXA_HUMAN	P20674 homo sapien
9	7	2.0	221	IFB3_ARATH	09fks9 arabidopsi
10	7	2.0	224	FLGA_YEREN	056892 yersinia en
11	7	2.0	224	MYOG_HUMAN	P15173 homo sapien
12	7	2.0	224	MYOG_MOUSE	P12179 mus musculu
13	7	2.0	224	MYOG_PIG	P49612 sus scrofa
14	7	2.0	249	Y382_NEIMA	091xg6 neisseria m
15	7	2.0	249	YK54_NEIMB	091xg9 neisseria m
16	7	2.0	250	YK24_PYRAB	09uvt3 pyrococcus
17	7	2.0	252	PGC4_ANASP	P29389 anabaena sp
18	7	2.0	278	Y3JC_SCHPO	094404 schizosacch
19	7	2.0	287	MYOG_RAT	P20428 rattus norv
20	7	2.0	291	RS2_TREPA	083155 treponema p
21	7	2.0	292	A36A_DROME	09k557 drosophila
22	7	2.0	301	SYGA_SHEON	08k655 sheanella
23	7	2.0	312	RLAO_YEAST	P03117 saccharomyc
24	7	2.0	322	PLGB_HUMAN	099645 homo sapien
25	7	2.0	328	PLS1_MOUSE	091100 mus musculu
26	7	2.0	330	YH75_ARCFU	028499 archaeoglob
27	7	2.0	335	PLS1_RAT	P15525 rattus norv
28	7	2.0	348	RLAO_HAIMA	P15525 halloarcu
29	7	2.0	398	GPDI_YARLI	09uvt4 yarrowia li
30	7	2.0	431	ARAL_BACHD	09kca6 bacillus ha
31	7	2.0	445	EXTL_STAM	099kx0 staphylococ
32	7	2.0	477	MMO3_HORSE	028397 equus cabal
33	7	2.0	502	YH60_MYCTU	006795 mycobacteri

34	7	2.0	507	YIR4_YEAST	P04486 saccharomyc
35	7	2.0	557	PAC1_PSEB3	P15557 pseudomonas
36	7	2.0	557	PAC1_PSEB3	005053 pseudomonas
37	7	2.0	577	UREI_MYCTU	P50042 mycobacteri
38	7	2.0	622	ABS_HUMAN	094v9 homo sapien
39	7	2.0	625	SYR_SULSO	0974n1 sulfolobus
40	7	2.0	641	SAC2_YEAST	P39904 saccharomyc
41	7	2.0	709	ANDR_RABIT	P49699 oryctolagus
42	7	2.0	775	PLSB_MYCLE	09x7b0 mycobacteri
43	7	2.0	825	PHK_SCHPO	074770 schizosacch
44	7	2.0	875	HIR2_YEAST	P32480 saccharomyc
45	7	2.0	884	ANDR_EULFC	097776 eulemur ful

## ALIGNMENTS

RESULT 1	ID	NEFL_HUMAN	STANDARD:	PRT:	350 AA.
AC	09GZT8	09H2D2; 09HC18;			
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DE	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	NIF3-like protein 1 (Amyotrophic lateral sclerosis 2 chromosomal				
DE	region candidate gene protein 1) (Miy018 protein) (MDS015).				
GN	NIF3L1 OR ALS2CR1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.				
RX	MEDLINE-20573864; PubMed-11124544;				
RA	Tascou S., Uedelhoven J., Dixkens C., Nayerula K., Engel W.,				
RA	Burfeind P.;				
RT	* Isolation and characterization of a novel human gene, NIF3L1, and its				
RT	mouse ortholog, Nif3l1, highly conserved from bacteria to mammals.;				
RL	Cytogenet. Cell Genet. 90:330-336(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-21100893; PubMed-11161814;				
RA	Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,				
RA	Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,				
RA	Ikedo J.-E., Hayden M.R.;				
RT	* Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,				
RT	and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)				
RL	critical region at chromosome 2q33-q34: candidate genes for ALS2.;				
RN	Genomics 71:200-213(2001).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RA	Mao Y.M., Xie Y., Huang X.Y., Ying K., Dai J.L.;				
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Huang C., Qian B., Yu Y., Gu W., Wang Y., Han Z., Chen Z.;				
RT	* Novel genes expressed in hematopoietic stem/progenitor cells from				
RT	myelodysplastic syndromes patient.;				
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Ovarian carcinoma;				
RA	Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,				
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,				
RA	Wagatsuna M., Hosofiri T., Kaku Y., Kodaira H., Kondo H.,				
RA	Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,				
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,				
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,				
RA	Ninomiyu K., Iwayanagi T.;				
RT	* NEO human cDNA sequencing project.;				
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.				
RN	[6]				

RP SEQUENCE FROM N.A.  
 RC TISSUE-Skin;  
 RA MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Collins F.S., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.J., Scheetz T.E.,  
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carinici P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE OPR0135 (NIF3) FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF283538; AAG44846.1; ALT\_INIT.  
 DR EMBL: AB038949; BAB32499.1; -  
 DR EMBL: AF060513; AAG43131.1; -  
 DR EMBL: AF182416; AAG14952.1; -  
 DR EMBL: AK023378; BAB14551.1; -  
 DR EMBL: BC007654; AAO7654.1; ALT\_INIT.  
 DR Genew: HGNC:13390; NIF3L.  
 DR InterPro: IPR002678; DUF34.  
 DR Pfam: PF01784; NIF3.1  
 DR TIGRFAMS: TIGR00486; TIGR00486.1.  
 DR CONFLICT 77 82 TWNTWK -> NIEHMR (IN REF. 4).  
 FT SEQUENCE 350 AA; 38983 MW; 81F1A5AD35B25ED7 CRC64;  
 SQ  
 Query Match 100.0%; Score 350; DB 1; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 301 ASOGINVLCEHSTNTERGFLSDLRMDLSHENKINIIITSETRDPLQV 350  
 RESULT 2  
 ID NIF3L\_MOUSE STANDARD; PRT; 350 AA.  
 AC OPR080; Q8D098;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NIF3-like protein 1.  
 GN NIF3L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RX MEDLINE=20573864; PubMed=11124544;  
 RA Tascou S., Uedelhoven J., Dikxens C., Nayeria K., Engel W.,  
 RA Burfelnd P.,  
 RT "Isolation and characterization of a novel human gene, NIF3L, and its  
 RT mouse orthology, Nif3l, highly conserved from bacteria to mammals.";  
 RL Cytogenet. Cell Genet. 90:330-336(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aitawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant H.,  
 RA Flitschmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustlincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,  
 RA Hayashaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- TISSUE SPECIFICITY: Ubiquitous.  
 CC -----  
 CC -1- SIMILARITY: BELONGS TO THE OPR0135 (NIF3) FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF284439; AAG45961.1; ALT\_INIT.  
 DR EMBL: AK011670; BAB27769.1; ALT\_INIT.  
 DR InterPro: IPR002678; DUF34.  
 DR MGD: MGI:1929485; Nif3l.  
 DR TIGRFAMS: TIGR00486; TIGR00486.1.  
 DR CONFLICT 164 164 G -> S (IN REF. 2).  
 FT CONFLICT 178 178 E -> K (IN REF. 2).  
 FT CONFLICT 191 191 L -> F (IN REF. 2).  
 FT CONFLICT 195 195 L -> Q (IN REF. 2).  
 FT CONFLICT 198 198 L -> F (IN REF. 2).  
 FT CONFLICT 208 208 T -> I (IN REF. 2).  
 FT SEQUENCE 350 AA; 38828 MW; B0FA71503CF7086 CRC64;

Query Match 14.6%; Score 51; DB 1; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-43;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKALLSLINDPASLSPAESMDNGLVLEPPPHVTNLTFLNDLTLEEVN 51  
 DB 1 MDKALLSLINDPASLSPAESMDNGLVLEPPPHVTNLTFLNDLTLEEVN 51

## RESULT 3

YF59\_STRAAM STANDARD; PRT; 366 AA.

ID YF59\_STRAAM STANDARD; PRT; 366 AA.  
 AC 099TT7;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Hypothetical protein SAV1559/SA1388.  
 GN SAV1559 OR SA1388.  
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and  
 OS Staphylococcus aureus (strain N315).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=158678, 158679;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Mu50 / ATCC 700699, and N315;  
 RX MEDLINE=21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 Rai L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,  
 RA Kanamori M., Matsumori H., Maruyama A., Murakami H., Hosoyma A.,  
 RA Mizutani-Ul Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,  
 RA Sekizima K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,  
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,  
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
 RT aureus".  
 RL Lancet 357:1225-1240(2001).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.  
 CC -----

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CC EMBL: AP003362; BAB57721.1; -;  
 DR EMBL: AP003362; BAB57721.1; -;  
 DR PIR: F89936; F89936.  
 DR InterPro: IPR002678; DUF34.  
 DR Pfam: PF01784; NIF3; 1.  
 DR TIGRPFAMs: TIGR00486; TIGR00486; 1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 366 AA; 41075 MW; CA7D5FADF78FFFA CRC64;

Query Match 2.9%; Score 10; DB 1; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.041;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 AESMDNVGILL 28  
 DB 19 AESMDNVGILL 28

## RESULT 4

NIF3\_YEAST STANDARD; PRT; 288 AA.

ID NIF3\_YEAST STANDARD; PRT; 288 AA.  
 AC P53081;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NG1-Interacting factor 3.

GN NIF3 OR YGL221C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C;  
 RX MEDLINE=97435481; PubMed=9290212;

RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.,  
 RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae  
 RT chromosome VII."  
 RL Yeast 13:1077-1090(1997).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.  
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DR EMBL: Z72743; CA96937.1; -;  
 DR PIR: S64243; S64243.  
 DR SGD: S0003189; NIF3.  
 DR InterPro: IPR002678; DUF34.  
 DR Pfam: PF01784; NIF3; 1.  
 DR TIGRPFAMs: TIGR00486; TIGR00486; 1.  
 SQ SEQUENCE 288 AA; 31888 MW; B6AB6E48A9A776A CRC64;

Query Match 2.6%; Score 9; DB 1; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 0.38;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 HSNTERGFL 320  
 DB 252 HSNTERGFL 260

## RESULT 5

RNA\_MYCPA STANDARD; PRT; 119 AA.

ID RNA\_MYCPA STANDARD; PRT; 119 AA.  
 AC 0917L9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase  
 DE P protein) (Protein C5).  
 GN RNA.

OS Mycobacterium paratuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1770;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Zhang Q., Kapur V.;  
 RT "Genomic organization of the Mycobacterium avium subsp.  
 RT paratuberculosis origin of replication region."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence  
 CC from pre-tRNA to produce the mature 5' terminus. It can also  
 CC cleave other RNA substrates such as 4.5S RNA. The protein  
 CC component plays an auxiliary but essential role in vivo by binding  
 CC to the 5'-leader sequence and broadening the substrate specificity  
 CC of the ribozyme (by similarity).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-  
 CC extra-nucleotide from tRNA precursor.  
 CC -1- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a  
 CC protein subunit (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE RNA FAMILY.

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DR EMBL; AF222789; AAF33695.1; -  
 DR HSSP; P25814; 1A6F.  
 DR HAMAP; MF\_00227; -; 1.  
 DR InterPro: IPR000100; Ribonuclease\_P.  
 DR Pfam; PF00825; Ribonuclease\_P; 1.  
 DR ProDom; PD003629; Ribonuclease\_P; 1.  
 DR TIGRFAMs; TIGR00188; rnpa; 1.  
 DR PROSITE; PS00648; RIBONUCLEASE\_P; 1.  
 KW Hydroxylase; Nuclease; Endonuclease; tRNA processing; RNA-binding.  
 SQ SEQUENCE 119 AA; 13131 MW; BBB6C38A11764721 CRC64;

Query Match 2.0%; Score 7; DB 1; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 RLVTAL 90  
 |||||  
 DB 85 RLVTAL 91

RESULT 6  
 SSBS\_XENLA STANDARD; PRT; 146 AA.  
 ID SSBS\_XENLA STANDARD; PRT; 146 AA.  
 AC P09380;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Single-stranded DNA-binding protein S, mitochondrial precursor (Mt-  
 DE SSB-S) (Mt-SSB 1).  
 GN MTSSB1.  
 OS Xenopus laevis (African clawed frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 CC Xenopodinae; Xenopus.  
 CC NCB1\_TaxID=8355;  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=91334145; PubMed=1870981;  
 RA Tiranat V., Barat-Gueride M., Bijl J., Didonato S., Zeviani M.;  
 RT "A full-length cDNA encoding a mitochondrial DNA-specific single-  
 RT stranded DNA binding protein from Xenopus laevis.";  
 RL Nucleic Acids Res. 19:4291-4291(1991).  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=97169147; PubMed=9016954;  
 RA Champagne A.M., Dufresne C., Viney L., Gueride M.;  
 RT "Cloning, sequencing and expression of the two genes encoding the  
 RT mitochondrial single-stranded DNA-binding protein in Xenopus  
 RT laevis.";  
 RL Gene 184:65-71(1997).  
 RN RP SEQUENCE OF 18-142.  
 RX MEDLINE=92061073; PubMed=1952953;  
 RA Ghir R., Lecaer J.-P., Dufresne C., Barat-Gueride M.;  
 RT "Primary structure of the two variants of Xenopus laevis mtSSB, a  
 RT mitochondrial DNA binding protein.";  
 RL Arch. Biochem. Biophys. 291:395-400(1991).  
 RN RP SEQUENCE OF 18-41.  
 RX MEDLINE=88296837; PubMed=3042458;  
 RA Mahoungou C., Ghir R., Lecaer J.-P., Mignotte B., Barat-Gueride M.;  
 RT "The amino-terminal sequence of the Xenopus laevis mitochondrial SSB  
 RT is homologous to that of the Escherichia coli protein.";  
 RL FEBS Lett. 235:267-270(1988).

CC -1- FUNCTION: This protein binds preferentially and cooperatively to  
 CC ss-DNA, and can under certain conditions stimulate the activity of  
 CC DNA polymerase. Probably involved in mitochondrial DNA  
 CC replication.  
 CC -1- SUBUNIT: Homotetramer (Probable).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE SSB FAMILY.

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DR EMBL; X59285; CAA41976.1; -  
 DR EMBL; X83673; CAA58647.1; -  
 DR PIR; JC6173; JC6173.  
 DR HSSP; Q04837; 30DL.  
 DR InterPro: IPR000424; SSB\_protein.  
 DR Pfam; PF00436; SSB; 1.  
 DR TIGRFAMs; TIGR00621; ssb; 1.  
 DR PROSITE; PS00735; SSB\_1; 1.  
 DR PROSITE; PS00736; SSB\_2; 1.  
 KW DNA-binding; DNA replication; Mitochondrion; Transit peptide.  
 FT TRANSIT 1  
 FT CHAIN 18 146  
 FT CHAIN 18 146  
 SQ SEQUENCE 146 AA; 16743 MW; F97D77149A255B3E CRC64;

Query Match 2.0%; Score 7; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 FLSDLD 325  
 |||||  
 DB 138 FLSDLD 144

RESULT 7  
 SSBR\_XENLA STANDARD; PRT; 148 AA.  
 ID SSBR\_XENLA STANDARD; PRT; 148 AA.  
 AC P09381; 013264;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Single-stranded DNA-binding protein R, mitochondrial precursor (Mt-  
 DE SSB-R) (Mt-SSB 2).  
 GN MTSSB2.  
 OS Xenopus laevis (African clawed frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 CC Xenopodinae; Xenopus.  
 CC NCB1\_TaxID=8355;  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=97169147; PubMed=9016954;  
 RA Champagne A.M., Dufresne C., Viney L., Gueride M.;  
 RT "Cloning, sequencing and expression of the two genes encoding the  
 RT mitochondrial single-stranded DNA-binding protein in Xenopus  
 RT laevis.";  
 RL Gene 184:65-71(1997).  
 RN RP SEQUENCE OF 18-99.  
 RX MEDLINE=92061073; PubMed=1952953;  
 RA Ghir R., Lecaer J.-P., Dufresne C., Barat-Gueride M.;  
 RT "Primary structure of the two variants of Xenopus laevis mtSSB, a  
 RT mitochondrial DNA binding protein.";  
 RL Arch. Biochem. Biophys. 291:395-400(1991).  
 RN RP PRELIMINARY SEQUENCE OF 18-38.  
 RX MEDLINE=88296837; PubMed=3042458;

RA Mahongou C., Ghir R., Lecaer J.-P., Mignotte B., Barot-Gueride M.;  
 RT "The amino-terminal sequence of the Xenopus laevis mitochondrial SSB  
 is homologous to that of the Escherichia coli protein.";  
 RL FEBS Lett. 235:267-270(1988).  
 CC -1- FUNCTION: This protein binds preferentially and cooperatively to  
 ss-DNA, and can under certain conditions stimulate the activity of  
 CC DNA polymerase. Probably involved in mitochondrial DNA  
 CC replication.  
 CC -1- SUBUNIT: Homotrimer (Probable).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: BELONGS TO THE SSB FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X83674; CAA58648.1; -  
 DR PIR: JC6172; JC6172.  
 DR HSSP: Q04837; 30UL.  
 DR InterPro: IPR000424; SSB\_protein.  
 DR Pfam: PF00436; SSB; 1.  
 DR TIGR: TIGR00621; ssb; 1.  
 DR PROSITE: PS00735; SSB\_1; 1.  
 DR PROSITE: PS00736; SSB\_2; 1.  
 KW DNA-binding; DNA replication; Mitochondrion; Transit peptide.  
 FT TRANSIT 1 17 MITOCHONDRION.  
 FT CHAIN 18 148 SINGLE-STRANDED DNA-BINDING PROTEIN R.  
 FT CONFLICT 49 49 D -> E (IN REF. 2).  
 SO SEQUENCE 148 AA; 16929 MW; 6DDA54C91779E803 CRC64;  
 OY Query Match 2.08; Score 7; DB 1; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 319 FLSDLRD 325  
 DB 140 FLSDLRD 146  
 ID COXA\_HUMAN STANDARD; PRT; 150 AA.  
 AC P20674; P30045;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va, mitochondrial precursor  
 DE (EC 1.9.3.1).  
 GN COX5A.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=89172069; PubMed=2853101;  
 RA Rizzuto R., Nakase H., Zeviani M., Dimauro S., Schon E.A.;  
 RT "Subunit Va of human and bovine cytochrome c oxidase is highly  
 RT conserved.";  
 RL Gene 69:245-256(1988).  
 RN [2]  
 RP SEQUENCE OF 42-52.  
 RC TISSUE=Liver;  
 RX MEDLINE=9417969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
 RA Tisot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993.";  
 RL Electrophoresis 14:1216-1222(1993).  
 RN [3]

RP SEQUENCE OF 56-64 AND 73-80.  
 RC TISSUE=Heart;  
 RX MEDLINE=96007936; PubMed=7498159;  
 RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,  
 RA Eshova E.S., Egorov T.A., Musalyanov A.K.;  
 RT "The major protein expression profile and two-dimensional protein  
 RT database of human heart.";  
 RL Electrophoresis 16:1160-1169(1995).  
 CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
 CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M22760; AAA99220.1; -  
 DR PIR: JT0342; OTHU5A.  
 DR SWISS-2DPAGE: P20674; HUMAN.  
 DR HSC-2DPAGE: P20674; HUMAN.  
 DR SienA-2DPAGE: P20674; -  
 DR GeneW: HGNC:2267; COX5A.  
 DR MIM: 603773; -  
 DR GO: GO:0004129; F:cytochrome c oxidase activity; TAS.  
 DR GO: GO:0005489; F:electron transporter activity; TAS.  
 DR InterPro: IPR003204; Cyt\_C-ox5A.  
 DR Pfam: PF02284; COX5A; 1.  
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane; Transit peptide.  
 FT TRANSIT 1 41 MITOCHONDRION.  
 FT CHAIN 42 150 CYTOCHROME C OXIDASE POLYPEPTIDE VA.  
 SO SEQUENCE 150 AA; 16774 MW; 84CDAF468BC9C85 CRC64;  
 OY Query Match 2.08; Score 7; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 10 LNDPAST 16  
 DB 99 LNDPAST 105  
 ID IFP3\_ARATH STANDARD; PRT; 221 AA.  
 AC G9PK59; O64928;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Eukaryotic translation initiation factor 4E type 3 (eIF-4E type 3)  
 DE (eIF4E type 3) (mRNA cap-binding protein type 3) (Novel cap-binding  
 DE protein) (ncBP).  
 GN AT5G18110 OR MG67.7.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxId=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98221164; PubMed=9553087;  
 RA Rud R.A., Kuhlman C., Goss D.J., Browning K.S.;  
 RT "Identification and characterization of a novel cap-binding protein  
 RT from Arabidopsis thaliana.";  
 RL J. Biol. Chem. 273:10325-10330(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-cv. Columbia;  
 RX MEDLINE-9840384; PubMed-9734815;  
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and TMC clones."  
 RL DNA Res. 5:203-216(1998).  
 RN [3].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-cv. Columbia;  
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
 RT "Riken Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
 RT SSP consortium (Salk/Stanford/PGSC)."  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Recognizes and binds the 7-methylguanosine-containing  
 CC mRNA "cap" during an early step in the initiation of protein  
 CC synthesis and facilitates ribosome binding by inducing the  
 CC unwinding of the mRNAs secondary structures.  
 CC -1- SUBUNIT: EIF4E is a trimer composed of EIF4E, EIF4G and EIF4A  
 CC (which can cycle in and out of the complex) (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AF028809; AAC17220.1; -  
 DR EMBL; AB012246; BAB09469.1; -  
 DR EMBL; AY092964; AAM12963.1; -  
 DR EMBL; AY093208; AAM13207.1; -  
 DR EMBL; AY114563; AAM47881.1; -  
 DR InterPro; IPR001040; TIF\_eif4E.  
 DR Pfam; PF01652; IF4E; 1.  
 DR PRODOM; PD003697; TIF\_eif4E; 1.  
 DR PROSITE; PS00813; IF4E; FALSE-NEG.  
 KW Initiation factor; Protein biosynthesis; RNA-binding;  
 KW Multigene family.  
 FT CONFIDENT 42 D -> L (IN REF. 1).  
 SQ SEQUENCE 221 AA; 25745 MW; FE484870E9769C6F CRC64;  
 Query Match 2.0%; Score 7; DB 1; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 242 IKRHLK 248  
 DB 187 IKRHLK 193  
 RESULT 10  
 FLGA\_YEREN  
 ID FLGA\_YEREN STANDARD; PRT; 224 AA.  
 AC Q56892;  
 DT 01-NOV-1997 (Rel. 35; Created)  
 DT 01-NOV-1997 (Rel. 35; Last sequence update)  
 DT 28-FEB-2003 (Rel. 41; Last annotation update)  
 DE Flagella basal body P-ring formation protein flga precursor.  
 GN Flag.  
 OS Yersinia enterocolitica.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=630;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-W1024 / Serotype O:9;  
 RA Fauconnier A., Allaoui A., van Elsen A., Cornelis G., Bollen A.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INVOLVED IN THE ASSEMBLY PROCESS OF THE P-RING

CC FORMATION. IT MAY ASSOCIATE WITH FLGE ON THE ROD CONSTITUTING A  
 CC STRUCTURE ESSENTIAL FOR THE P-RING ASSEMBLY (BY ACT AS A  
 CC MODULATOR PROTEIN FOR THE P-RING ASSEMBLY (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (probable).  
 CC -1- SIMILARITY: BELONGS TO THE FLGA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; 248169; CAA88191.1; -  
 DR PIR; S54218; S54218.  
 DR InterPro; IPR004924; FLGA.  
 DR Pfam; PF03240; FLGA; 1.  
 KW Flagella; Periplasmic; Signal.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 224 FLAGELLIN BASAL BODY P-RING FORMATION  
 FT PROTEIN FLGA.  
 SQ SEQUENCE 224 AA; 24351 MW; B98B74FBC7862A49 CRC64;  
 Query Match 2.0%; Score 7; DB 1; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 262 ESQVKV 268  
 DB 45 ESQVKV 51  
 RESULT 11  
 MYOG\_HUMAN  
 ID MYOG\_HUMAN STANDARD; PRT; 224 AA.  
 AC P15173;  
 DT 01-APR-1990 (Rel. 14; Created)  
 DT 01-DEC-1992 (Rel. 24; Last sequence update)  
 DT 15-SEP-2003 (Rel. 42; Last annotation update)  
 DE Myogenin (Myogenic factor Myf-4).  
 GN MYOG OR MYF4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92064650; PubMed-1659574;  
 RA Salminen A., Braun T., Buchberger A., Juers S., Winter B.,  
 RA Arnold H.H.;  
 RT "Transcription of the muscle regulatory gene Myf4 is regulated by  
 RT serum components, peptide growth factors and signaling pathways  
 RT involving G proteins."  
 RL J. Cell Biol. 115:905-917(1991).  
 RN [2]  
 RP PRELIMINARY SEQUENCE FROM N.A.  
 RC TISSUE-Skeletal muscle;  
 RX MEDLINE-90059960; PubMed-2583111;  
 RA Braun T., Bober E., Buschhausen-Denker G., Kohz S., Grzeschik K.-H.,  
 RA Arnold H.H.;  
 RT "differential expression of myogenic determination genes in muscle  
 RT cells: possible autoactivation by the Myf gene products."  
 RL EMBO J. 8:3617-3625(1989).  
 RN [3]  
 RP REVISIONS.  
 RA Braun T., Bober E., Buschhausen-Denker G., Kohz S., Grzeschik K.-H.,  
 RA Arnold H.H.;  
 RL EMBO J. 9:592-592(1990).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Muscle;  
 RX MEDLINE-22388257; PubMed-12477932;

RA Strausberg R.L., Felding A.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,  
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: INVOLVED IN MUSCLE DIFFERENTIATION (MYOGENIC FACTOR).  
CC INDICES FIBROBLASTS TO DIFFERENTIATE INTO MYOBLASTS. PROBABLE  
CC SEQUENCE SPECIFIC DNA-BINDING PROTEIN.  
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another  
CC BHLH protein.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: X62155; CAA44080.1; -;  
DR EMBL: X17651; CAA35641.1; ALT\_SEQ.  
DR EMBL: BC006347; AA06347.1; -;  
DR PIR: A41128; A41128.  
DR HSSP: P10085; IMDY.  
DR TRANSFAC: T00520; -;  
DR Genew: HGNC:7612; MYOG.  
DR MIM: 159980; -;  
DR GO: GO:0003700; F:transcription factor activity; TAS.  
DR GO: GO:0007519; P:myogenesis; TAS.  
DR InterPro: IPR002546; Basic.  
DR InterPro: IPR001092; HLH\_Basic.  
DR Pfam: PF01586; Basic; 1.  
DR Pfam: PF00010; HLH; 1.  
DR SMART: SM00520; BASIC; 1.  
DR SMART: SM00353; HLH; 1.  
DR PROSITE: PS00038; HLH\_1; 1.  
DR PROSITE: PS00888; HLH\_2; 1.  
DR Myogenesis; Differentiation; Developmental protein; Nuclear protein;  
KW DNA-binding.  
FT DNA\_BIND 81 93 BASIC DOMAIN  
FT SEQUENCE 224 AA; 25037 MW; 91421D5B5751FB CRC64;  
SQ  
Query Match 2.0%; Score 7; DB 1; Length 224;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P12979;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Myogenin (MYO1-related protein).  
GN MYOG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE=Muscle;  
RX MEDLINE=89306601; PubMed=2473006;  
RA Edmondson D.G., Olson E.N.;  
RT "A gene with homology to the myc similarity region of MyoD is  
RT expressed during myogenesis and is sufficient to activate the muscle  
RT differentiation program.";  
RL Genes Dev. 3:628-640(1989).  
RN [2]  
RP ERRATUM.  
RX MEDLINE=91032996; PubMed=2172083;  
RA Edmondson D.G., Olson E.N.;  
RN Genes Dev. 4:1450-1450(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92375033; PubMed=1324403;  
RA Edmondson D.G., Cheng T.C., Cserjesi P., Chakraborty T., Olson E.N.;  
RT "Analysis of the myogenin promoter reveals an indirect pathway for  
RT positive autoregulation mediated by the muscle-specific enhancer  
RT factor MEF-2.";  
RL Mol. Cell. Biol. 12:3665-3677(1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90368705; PubMed=2168405;  
RA Fujisawa-Senara A., Nabeshima Y., Hosoda Y., Ohtsuka T., Nabeshima Y.;  
RT "Myogenin contains two domains conserved among myogenic factors.";  
RL J. Biol. Chem. 265:15219-15223(1990).  
CC -1- FUNCTION: INVOLVED IN MUSCLE DIFFERENTIATION (MYOGENIC FACTOR).  
CC INDICES FIBROBLASTS TO DIFFERENTIATE INTO MYOBLASTS. PROBABLE  
CC SEQUENCE SPECIFIC DNA-BINDING PROTEIN.  
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another  
CC BHLH protein.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: M95800; AAB59676.1; -;  
DR EMBL: X15784; CAA33785.1; ALT\_SEQ.  
DR EMBL: D90156; BAA1487.1; -;  
DR PIR: A35882; A36675.  
DR HSSP: P10085; IMDY.  
DR TRANSFAC: T00528; -;  
DR MGD: MGI:97276; Myog.  
DR InterPro: IPR002546; Basic.  
DR InterPro: IPR001092; HLH\_Basic.  
DR Pfam: PF01586; Basic; 1.  
DR Pfam: PF00010; HLH; 1.  
DR SMART: SM00520; BASIC; 1.  
DR SMART: SM00353; HLH; 1.  
DR PROSITE: PS00038; HLH\_1; 1.  
DR PROSITE: PS00888; HLH\_2; 1.  
DR Myogenesis; Differentiation; Developmental protein; Nuclear protein;  
KW DNA-binding.  
FT DNA\_BIND 81 93 BASIC DOMAIN



FT DOMAIN 94 133 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
 SQ SEQUENCE 224 AA; 25203 MW; CC7352C1EDF9D3D8 CRC64;  
 Query Match 2.0%; Score 7; DB 1; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ALLSLN 11  
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 Db 134 ALLSLN 140

RESULT 13  
 ID MYOG\_PIG STANDARD; PRT; 224 AA.  
 AC P49812;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Myogenin.  
 GN MYOG.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 CX NCBI\_Taxid=9623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Briley G.P., Reedy J.M., Grant A.L., Bidwell C.A.;  
 RL submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Soumillion A., Erkens J.H.F., Lenstra J.A., Zilstra C.,  
 RA Bosma A.A., Te Pas M.F.W.;  
 RL submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: INVOLVED IN MUSCLE DIFFERENTIATION (MYOGENIC FACTOR).  
 CC INDUCES FIBROBLASTS TO DIFFERENTIATE INTO MYOBLASTS. PROBABLE  
 CC SEQUENCE SPECIFIC DNA-BINDING PROTEIN.  
 CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another  
 CC BHLH protein.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 CC TRANSCRIPTION FACTORS. "MYOGENIC FACTORS" SUBFAMILY.  
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 CC -----  
 CC EMBL: U14331; AAB97306.1; -  
 DR EMBL: X89007; CAA61410.1; -  
 DR HSSP: P10085; IMDY.  
 DR InterPro: IPR002546; Basic.  
 DR InterPro: IPR001092; HLH\_basic.  
 DR Pfam: PF01586; Basic; 1.  
 DR Pfam: PF00010; HLH; 1.  
 DR SMART: SMO0520; BASIC; 1.  
 DR SMART: SMO0353; HLH; 1.  
 DR PROSITE: PS00038; HLH\_1; 1.  
 DR PROSITE: PS50888; HLH\_2; 1.  
 KW Myogenesis; Differentiation; Developmental protein; Nuclear protein;  
 KM DNA-binding.  
 FT DNA\_BIND 81 93 BASIC DOMAIN.  
 FT DOMAIN 94 133 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
 SQ SEQUENCE 224 AA; 25085 MW; 29A12219ACBF2B5 CRC64;

Query Match 2.0%; Score 7; DB 1; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ALLSLN 11  
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 Db 134 ALLSLN 140

RESULT 14  
 ID Y382\_NEIMA STANDARD; PRT; 249 AA.  
 AC O9JWG6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein NMA0382.  
 GN NMA0382.  
 OS Neisseria meningitidis (serogroup A).  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 CC Neisseriaceae; Neisseria.  
 CX NCBI\_Taxid=65699;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;  
 RX MEDLINE=20222556; PubMed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,  
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,  
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 RA Whitehead S., Spratt B.G., Barrall B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria  
 RT meningitidis Z2491.";  
 RL Nature 404:502-506(2000).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.  
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 CC -----  
 CC EMBL: AL162753; CAB83683.1; -  
 DR PIR: D81954; D81954.  
 DR InterPro: IPR002678; DUF34.  
 DR Pfam: PF01784; NIF3; 1.  
 DR TIGRPFAMs: TIGR00486; TIGR00486; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 249 AA; 27484 MW; FDE2EE1B3FC216F CRC64;

Query Match 2.0%; Score 7; DB 1; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 DLYTNGE 291  
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 Db 190 DLYTNGE 196

RESULT 15  
 ID YK34\_NEIMB STANDARD; PRT; 249 AA.  
 AC O9JXG9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein NMB2054.  
 GN NMB2054.  
 OS Neisseria meningitidis (serogroup B).  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 CC Neisseriaceae; Neisseria.  
 CX NCBI\_Taxid=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.



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RC STRAIN-MC58 / Serogroup B;
RX MEDLINE-20175755; PubMed-10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gall J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT *Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.*;
RL Science 287:1809-1815(2000).
CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
CC -----
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CC -----
CC EMBL: AE002555; AAF42374.1; -
DR PIR: G81011; G81011.
DR TIGR: NMB2054; -
DR InterPro: IPR002678; DUF34.
DR Pfam: PF01784; NIF3; 1
DR TIGRPFAM: TIGR00486; TIGR00486; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 249 AA; 27417 MW; 58EC0E47B6AE27B2 CRC64;

Query Match 2.0%; Score 7; DB 1; Length 249;
Best local Similarity 100.0%; Pred No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 285 DLYLTGE 291
|||
Db 190 DLYLTGE 196

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